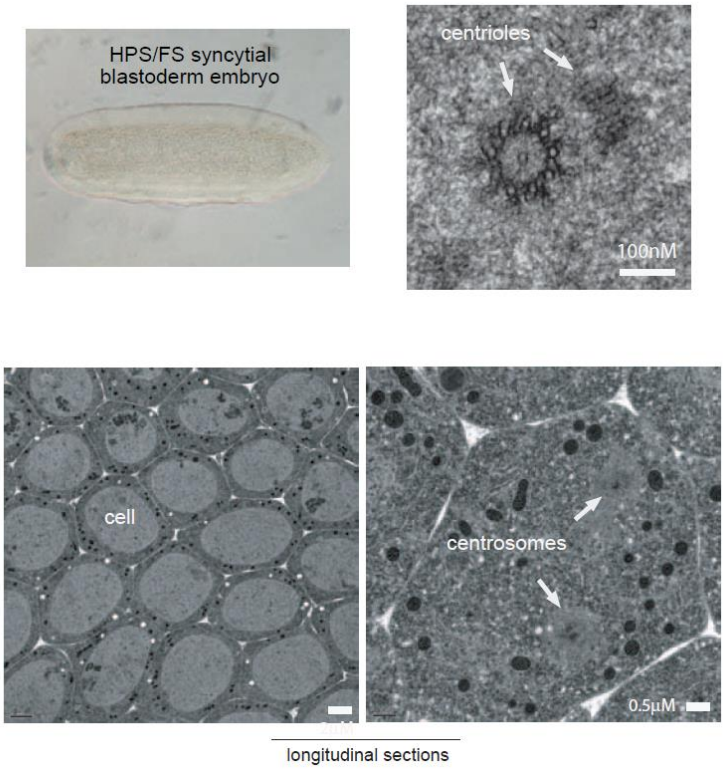

Figure S1 a) High-pressure frozen and freeze-substituted *Drosophila* embryos from syncytial blastoderm stage embedded with Epon resin were used to assess the preservation of the tissue for EM immunostaining shown in Fig.1e (See Methods).

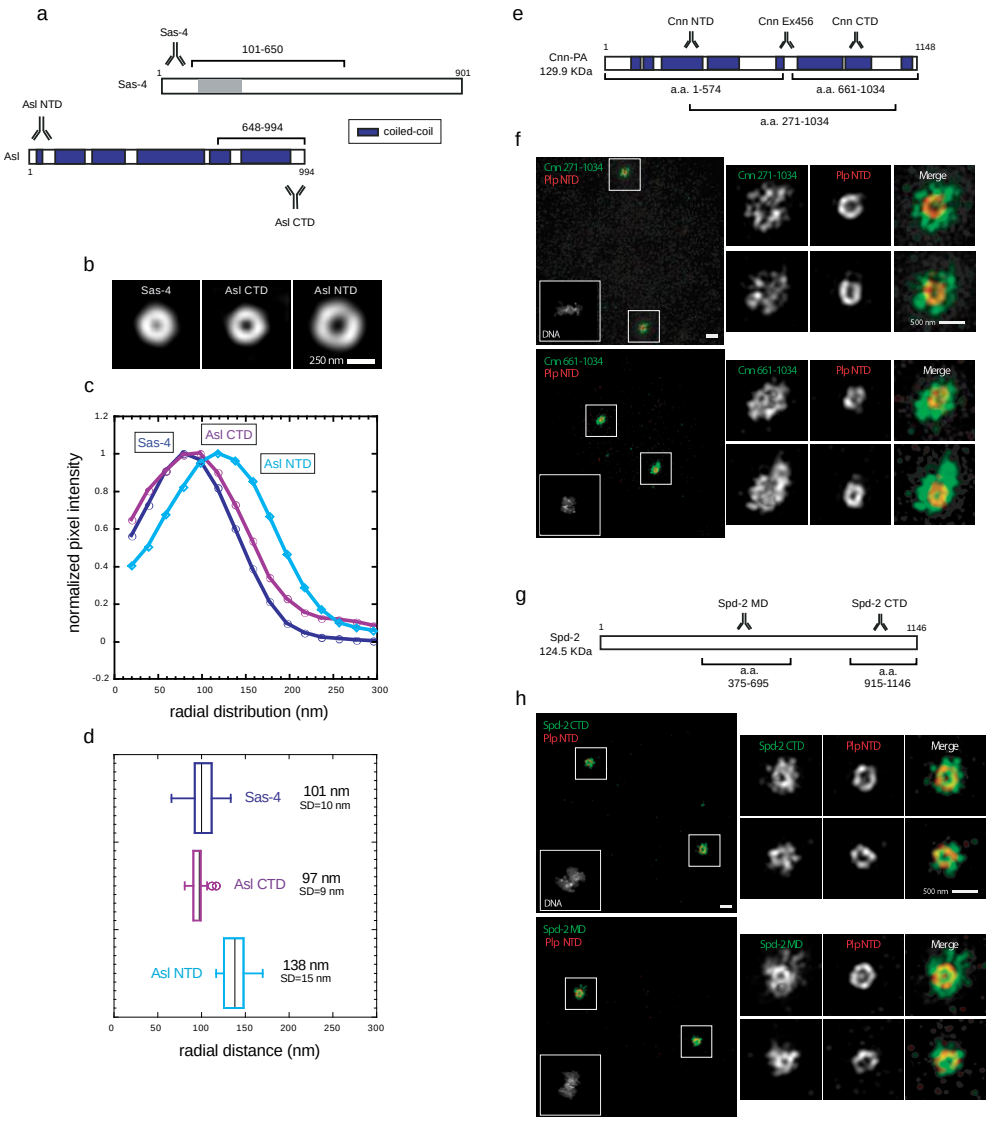

Figure S2 a) Linear map of *Drosophila* Asl and Sas-4 with interaction region obtained from Dzhindzhev, Yu et al. 2010. Sequence prediction of coiled-coil conformation was obtained with the software Coils. The antibodies located above amino-acid map show the position of the protein sequence used for immunization (see also Sup Fig.1a). b) 2D projections of the aligned volumes average. (Sas-4 n=68; Asl CTD n=21; Asl NTD n=21). c) Fluorescence intensities profiles from the center of the centriole image outward measured from radially averaged 2D projections of average volumes of the specified centrosomal proteins. d) Radially averaged fluorescence intensities values from projected volumes were fitted to an offset mirrored Gaussian function to calculate the center position of the distribution of individual centrosomal proteins and domains. e) Linear map of the amino-acid sequence of *Drosophila* Cnn-PA obtained from the Flybase database. Sequence prediction of coiled-coil conformation was performed with the software Coils with a window of 28 residues. Amino-acid stretches were considered coiled-coil if predicted with a probability of 70% or higher. f) S2 cells stained with either rabbit anti-Cnn antibodies against 271-1034 or rabbit anti-Cnn 611-1024 (anti-rabbit Alexa 488 secondary antibodies) and anti-Plp NTD (anti-guineapig 555 secondary antibodies). Dna was labeled with DAPI stain. See Fig. 5c and Sup Fig. 3c for distribution of anti-Cnn 1-576. Scale bar 1 µm. g) Linear map of the amino-acid sequence of *Drosophila* Spd-2 obtained from the Flybase database. Sequence prediction of coiled-coil conformation was performed with the software Coils (see above). h) S2 cells stained with either rabbit anti-Spd-2 antibodies against 375-695 or rabbit anti-Spd-2 915-1146 (anti-rabbit Alexa 488 secondary antibodies) and anti-Plp NTD (anti-guineapig 555 secondary antibodies). Dna was labeled with DAPI. Scale bar 1 µm.

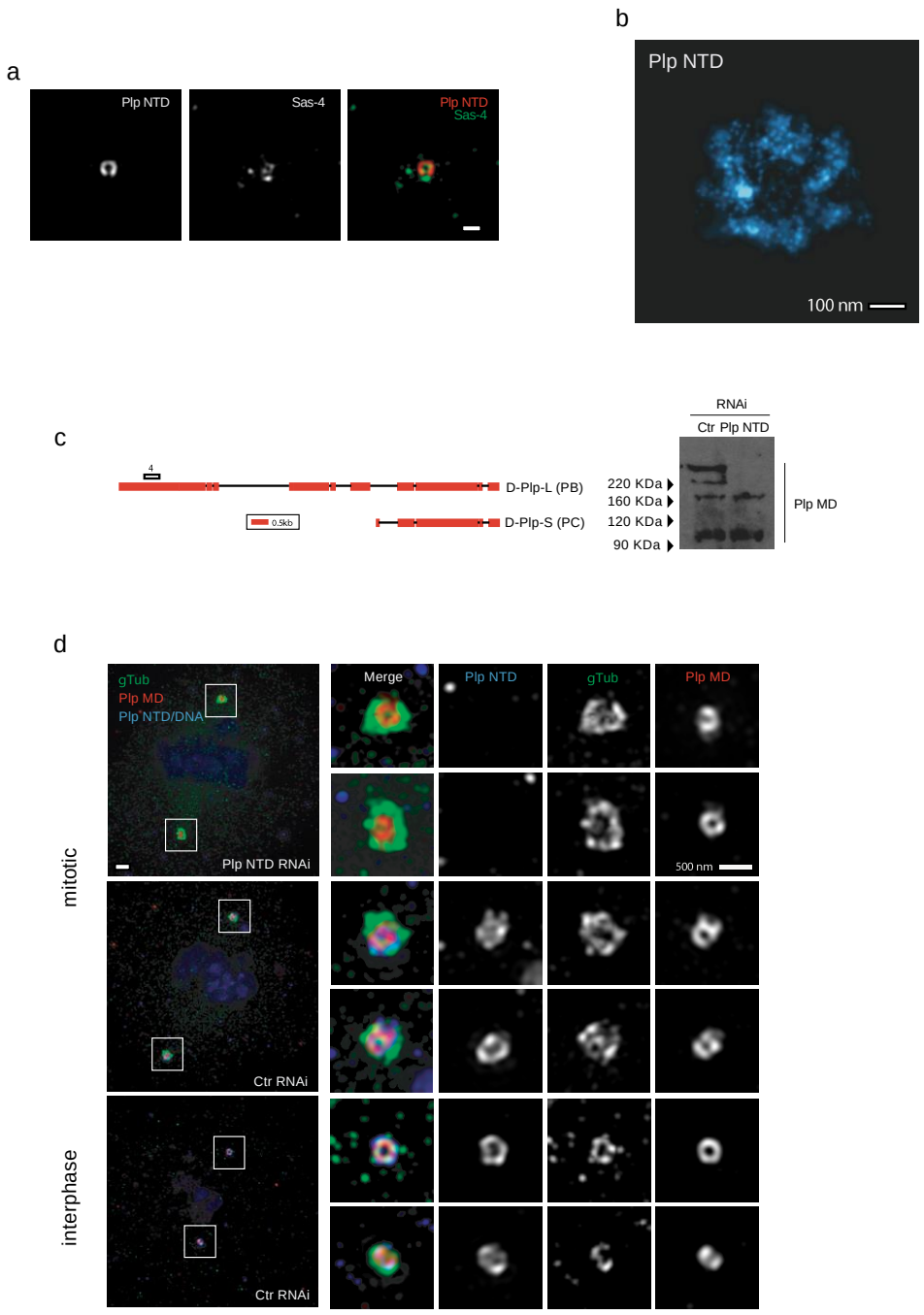

Figure S3 a) Centrosomes biochemically isolated from *Drosophila* syncytial blastoderm embryos stained with anti-Plp NTD or anti-Sas-4 antibodies. Scale bar 500 nm. b) STORM image of a centriole from S2 cells labeled with anti-Plp NTD antibody and anti-rabbit secondary antibodies conjugated with Alexa 647/Alexa 405 dye pairs. Note the elongated distribution of Plp clusters. c) Left, Plp genomic region obtained from Flybase database (5' and 3' UTR regions are not displayed). The position of the sequences on Plp exons used for dsRNA production is annotated on the sequence. Right, western blot on extracts obtained from S2 cells treated for ctr or Plp NTD dsRNA. d) S2 cells treated with dsRNA against Plp exon 1 were stained with anti-Plp NTD (anti-guineapig 405) and MD (anti-rabbit 555) together with anti-gTubulin antibodies (anti-mouse 488 conjugated). Dna was labeled with DAPI stain. Images were acquired in the camera linear range of response and are displayed with identical intensity settings. When we stain cells with only g-tubulin antibody we obtain similar distribution to the ones from triple labeled cells shown here, thus ruling out any putative bleed through. Scale bar 1 µm.

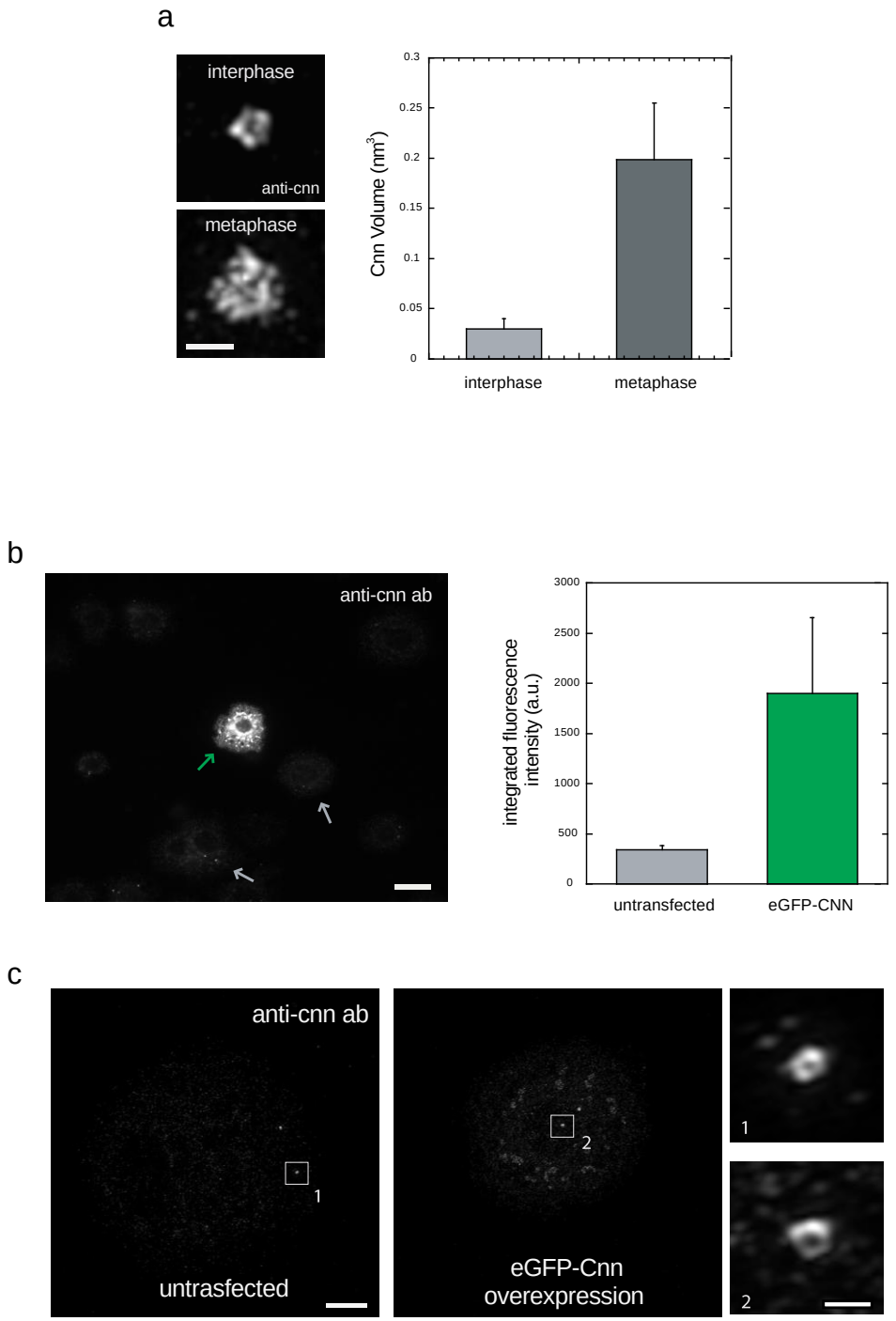

Figure S4 a) Left. SIM images of centrosomes in intephase (top) or metaphase (bottom) stained with anti-Cnn antibodies (1-576). Right. Analysis of volume size of centrosomes stained with anti-Cnn antibodies in interphase or metaphase. b) Representative example of S2 cells transfected with eGFP-Cnn (green arrow) used for analysis. White arrows point at untransfected cells. Right, quantification of Cnn levels in wild type S2 cells or after transfection with eGFP-Cnn plasmid. c) Examples of localization of Cnn in transfected vs untransfected cells. Note that the images intensities are scaled differently in the bottom panel to allow proper visualization of eGFP-Cnn overexpressing cells. Scale bar left 5 µm, right 500 nm.

Table S1 a) Summary table of the measurements of center position (xc) and width distribution (s) of the fluorescence intensities obtained from individual centrosomal protein volumes stained with the specified antibodies.